AMENDMENTS TO THE CLAIMS

1. (Original) A method to detect [a NF-κB related medical condition] Incontinentia Pigmenti in [an organism] a human comprising the steps of:

obtaining a sample from said organism; and

analyzing said sample for an alteration in a nucleic acid of SEQ ID NO:1[, wherein said alteration results in inactivation of NF-κB].

2. (Original) The method of Claim 1, wherein said alteration is a mutation, wherein said mutation is selected from the group consisting of a deletion, an insertion, a point mutation, a rearrangement in said sequence, and a combination thereof.

3. (Original) The method of Claim 2, wherein said point mutation is selected from the group consisting of a nonsense mutation, a frameshift mutation, a missense mutation, a splicing-related mutation, and a combination thereof.

4. (Original) The method of Claim 1, wherein said alteration is located in a regulatory nucleic acid, a promoter nucleic acid an exon, an intron, an initiator codon, a stop codon, an exon/intron junction, a 5′ untranslated region, a 3′ untranslated region and a combination thereof.

5. (Original) The method of Claim 1, wherein said analyzing step comprises a method selected from the group consisting of hybridization, SSCP, heteroduplex analysis, sequencing, polymerase chain reaction, electrophoresis, and a combination thereof.

6-8. (Cancel)

9-31. (Previously Cancelled)

32. (Original) A method to detect an alteration in a nucleic acid of SEQ ID NO:1 in an organism, comprising the steps of:

obtaining a sample from said organism; and

analyzing said sample for said alteration.

33. (Original) The method of Claim 32, wherein said alteration is a mutation, wherein said mutation is selected from the group consisting of a deletion, an insertion, point mutation, a rearrangement, and a combination thereof.

34. (Original) The method of Claim 33, wherein said point mutation is selected from the group consisting of a nonsense mutation, a frameshift mutation, a missense mutation, a splicing-related mutation, and a combination thereof.

35. (Original) The method of Claim 32, wherein said alteration is located in a regulatory nucleic acid, a promoter nucleic acid, an exon, an intron, an initiator codon, a stop codon, an exon/intron junction, a 5′ untranslated region, a 3′ untranslated region and a combination thereof.

36. (Original) The method of Claim 32, wherein said analyzing step comprises a method selected from the group consisting of hybridization, SSCP, heteroduplex analysis, sequencing, polymerase chain reaction, electrophoresis, and a combination thereof.

37. (Original) The method of Claim 32, wherein said organism is a human.

38. (Original) The method of Claim 32, wherein said organism is a human selected from the group consisting of an affected individual, a carrier individual, or a noncarrier individual.

39. (Original) The method of claim 32, wherein said analyzing step further comprises a technique selected from the group consisting of PCR analysis and Southern blot analysis.

40-42. (Previously Cancelled)

43. (Original) The method of Claim 39, wherein a probe for said Southern analysis is a nucleic acid of SEQ ID NO:3, or fragments and derivatives thereof.

Claims 44-49. (Previously Cancelled)

50. (Cancel)

51. (Previously Added) A method to detect Incontinentia pigmenti in [an organism] a human comprising the steps of:

obtaining a sample from said organism; and

analyzing said sample for an alteration in a human NEMO nucleic acid.

52. (New) The method of claim 1, wherein said alteration results in inactivation of NF-κB.

53. (New) The method of claim 52, wherein said alteration is in an exon.